

## BEST AVAILABLE COPY



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

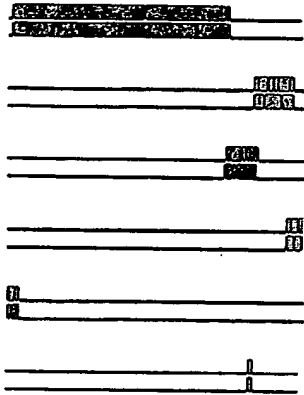
Taxonomy

Structure

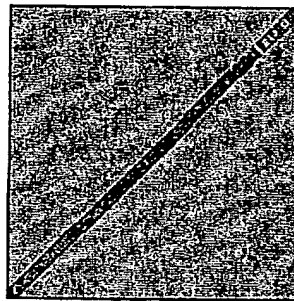
## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☐

Sequence gi 14545110 Sequence 1 from Patent WO0138564. Length 8378 (1 .. 8378)  
 1  
 Sequence gi 1041088 Rattus norvegicus sodium channel I mRNA, complete cds. Length 8399 (1 .. 8399)  
 2



2



1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 8241 bits (4286), Expect = 0.0  
 Identities = 5554/6183 (89%), Gaps = 6/6183 (0%)  
 Strand = Plus / Plus

```
Query:      169  gggatgatgctgttcctcactgcagatggataattttccttttaatacaggaatttcatatg 228
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:      155  gggagatgttggttccttactgcagatagataattttccttttatcaggaatctcacatg 214
```

```
Query:      229  cagaataaatggtaattaaaatgtgcaggatgacaagatggagcaaacagtgttgtacc 288
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Sbjct:      215  aagagtaaagagtaattaaaatgtgcaggatgacaagatggagcaaacagtgttgtacc 274
Na+ channel 1                                     M E Q T V L V P
```

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Query:      289  accaggacctgacagcttcaacttcttcaccagagaatctcttgcggtattgaaagacg 348
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:      275  accaggacctgacagcttcaacttcttcaccagagaatctcttgagctattgaaaggcg 334
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Na+ channel 9      P G P D S F N F F T R E S L A A I E R R

Query:      349    cattgcagaagaaaaggcaaagaatcccaaaccagacaaaaaagatgacgacgaaaatgg 408  
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Sbjct:      335    cattgcagaagaaaagctaagaatcccaagccagacaaaaaagatgatgatgaaaatgg 394  
Na+ channel 29      I A E E K A K N P K P D K K D D D E N G

Query:      409    cccaaagccaaatagtgcacttgggaagctgggaagaaccttccatttatttatggagacat 468  
              |||||  
Sbjct:      395    cccaaagccgaacagtgcacttgggaagctgggaagaaccttccatttatttatggagacat 454  
Na+ channel 49      P K P N S D L E A G K N L P F I Y G D I

Query:      469    tcctccagagatggtgtcagagccctggaggacctggaccctactatatcaataagaa 528  
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Sbjct:      455    tcctccagagatggtgtcggagcctctggaggacctggaccctactatatcaataagaa 514  
Na+ channel 69      P P E M V S E P L E D L D P Y Y I N K K

Query:      529    aacttttatagtattgaataaagggaaggccatcttccggttcagtgccacctctgcct 588  
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Sbjct:      515    aacttttatagtattgaataaagggaaggccatcttccggttcagtgccacctctgcct 574  
Na+ channel 89      T F I V L N K G K A I F R F S A T S A L

Query:      589    gtacattttaactcccttcaatcctcttaggaaaaatagctattaagattttggtacattc 648  
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Sbjct:      575    gtacattttaactcccttcaatcctcttaggaaaaatagctattaagattttggtacattc 634  
Na+ channel 109      Y I L T P F N P L R K I A I K I L V H S

Query:      649    attattcagcatgctaattatgtgcactattttgacaaactgtgtgtttatgacaatgag 708  
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Sbjct:      635    attattcagcatgttaattatgtgcactattttgacgaactgtgtatttatgacaatgag 694  
Na+ channel 129      L F S M L I M C T I L T N C V F M T M S

Query:      709    taaccctcctgattggacaaagaatgtagaatacaccttcacaggaatatatacttttga 768  
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Sbjct:      695    taaccctcctgactggacaaagaatgtagagtacaccttcacaggaatatatacttttga 754  
Na+ channel 149      N P P D W T K N V E Y T F T G I Y T F E

Query:      769    atcacttataaaaattattgcaaggggattctgtttagaagattttactttccttcggga 828  
              |||||  
Sbjct:      755    atcactaataaaaattattgcaaggggcttctgtttagaagattttactttccttcgtga 814  
Na+ channel 169      S L I K I I A R G F C L E D F T F L R D

Query:      829    tccatggaactggctcgatttcactgtcattacatttgcgtagctcacagagtttgtgga 888  
              |||||  
Sbjct:      815    cccatggaactggctggacttcactgtcattacattcgcatatgtgacggagtttgtgga 874  
Na+ channel 189      P W N W L D F T V I T F A Y V T E F V D

Query:      889    cctgggcaatgtctcggcattgagaacattcagagttctccgagcattgaagacgatttc 948  
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Sbjct:      875    cctgggcaatgtctcagcgttgagaacattcagagttcttcgagcattgaaaacaatatc 934

Na+ channel 209 L G N V S A L R T F R V L R A L K T I S

Query: 949 agtcattccaggcctgaaaaccattgtgggagccctgatccagtcctgtgaagaagctctc 1008  
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Sbjct: 935 agtcattccaggcctgaagaccatcggtggggccctgatccagtcctgtgaagaagctctc 994  
Na+ channel 229 V I P G L K T I V G A L I Q S V K K L S

Query: 1009 agatgtaatgacccctgactgtgttctgtctgagcgtatttgctctaattgggctgcagct 1068  
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Sbjct: 995 tgacgtcatgacccctcaccgtgttctgtctcagtggtttgctctaattcggttgagct 1054  
Na+ channel 249 D V M I L T V F C L S V F A L I G L Q L

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Sbjct: 1055 ttcatgggcaacctgaggaataagtgtgtacagtggccccccaccaacgcttccttgga 1114  
Na+ channel 269 F M G N L R N K C V Q W P P T N A S L E

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Na+ channel 289 E H S I E K N V T T D Y N G T L V N E T

Query: 1189 tgtctttgagtttgactggaagtcataatattcaagattcaagatatcattatttcctgga 1248  
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Sbjct: 1175 cgtgtttgaatttgactggaatcatacattcaagactcaagatatcattatttcctgga 1234  
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Na+ channel 329 G V L D A L L C G N S S D A G Q C P E G

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Na+ channel 369 S W A F L S L F R L M T Q D F W E N L Y

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06/17/2004



Na+ channel 1009 M N N L Q I A V D R M H K G V A Y V K R

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Na+ channel 1129 T E D F S S E S D L E E S K E K L N E S

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Na+ channel 1149 S S S S E G S T V D I G A P A E E Q P V

Query: 3769 agtggaaacctgaagaaactcttgaaccagaagcttgtttcactgaaggctgtgtacaaag 3828  
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Na+ channel 1309 L G A I K S L R T L R A L R P L R A L S

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Na+ channel 1329 R F E G M R V V V N A L L G A I P S I M

Query: 4308 gaatgtgcttctggtttgtcttatattctggctaattttcagcatcatgggcgtaaattt 4367  
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Query: 4368 gtttgctggcaaattctaccactgtattaacaccacaactggtgacaggttgacatcga 4427  
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Na+ channel 1369 F A G K F Y H C V N T T T G D T F E I T

Query: 4428 agacgtgaataatcatactgattgcctaaaactaatagaaagaaatgagactgctcgatg 4487  
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Sbjct: 4415 cgaagtcaataatcattctgattgcctaaaactaatagaaagaaatgagactgcccgtg 4474  
Na+ channel 1389 E V N N H S D C L K L I E R N E T A R W

Query: 4488 gaaaaatgtgaaagtaaactttgataatgtaggatttgggtatctctctttgcttcaagt 4547  
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Sbjct: 4475 gaaaaatgtgaaagtaaactttgataatgtaggatttgggtatctctctttgcttcaagt 4534



06/17/2004

Na+ channel 1609 F V V V I L S I V G M F L A E L I E K Y

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Sbjct: 5135 tttcgtgtccccctaccctgttccgagtcacccgctggccaggattggacgaatcctacg 5194  
Na+ channel 1629 F V S P T L F R V I R L A R I G R I L R

Query: 5208 tctgatcaaaggagcaaaggggatccgcacgtgctctttgctttgatgatgtcccttcc 5267  
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Na+ channel 1649 L I K G A K G I R T L L F A L M M S L P

Query: 5268 tgcgttggtttaacatcgccctcctactcttcttagtcatgttcatctacgccatctttgg 5327  
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Na+ channel 1669 A L F N I G L L L F L V M F I Y A I F G

Query: 5328 gatgtccaactttgcctatgttaagaggggaagttgggatcgatgacatgttcaactttga 5387  
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Sbjct: 5315 gatgtccaactttgcctatgttaagaggggaagttggaattgatgacatgttcaactttga 5374  
Na+ channel 1689 M S N F A Y V K R E V G I D D M F N F E

Query: 5388 gacctttggcaacagcatgatctgcctattccaaattacaacctctgctggctgggatgg 5447  
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Sbjct: 5375 gacttttggcaacagcatgatctgcctgttccaaatcaccacctctgctgggctgggacgg 5434  
Na+ channel 1709 T F G N S M I C L F Q I T T S A G W D G

Query: 5448 attgctagcaccattctcaacagtaagccacccgactgtgaccctaataaagttaaccc 5507  
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Query: 5568 ttacatcatcatatccttctggttggtgaacatgtacatcgcggtcatcctggagaa 5627  
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Na+ channel 1769 Y I I I S F L V V V N M Y I A V I L E N

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Query: 5688 ctatgaggtttgggagaagtttgatcccgatgcaactcagttcatggaatttgaaaaatt 5747  
|||||  
Sbjct: 5675 ctacgaggtctgggagaagttcgaccctgacgccactcagttcatggaatttgaaaaatt 5734

Na+ channel 1809 Y E V W E K F D P D A T Q F M E F E K L

Query: 5748 atctcagtttgcagctgcgcttgaaccgcctctcaatctgccacaaccaaactcca 5807  
|||||  
Sbjct: 5735 atctcagtttgcagctgctctcgaacccctctcaacttaccacaacccaacttca 5794  
Na+ channel 1829 S Q F A A A L E P P L N L P Q P N K L Q

Query: 5808 gctcattgccatggatttgcctatgggtgagtggtgaccggatccactgtcttgatatctt 5867  
|||||  
Sbjct: 5795 gctcattgccatggacctgccccatgggtgagtggtgagaccgcatccactgcctggacatctt 5854  
Na+ channel 1849 L I A M D L P M V S G D R I H C L D I L

Query: 5868 atttgcttttacaaagcgggttctaggagagagtggtgagagatggatgctctacgaataca 5927  
|||||  
Sbjct: 5855 gtttgcttttacaaagcgggttctggcgagagtggtgagagatggacgctcttcgaatcca 5914  
Na+ channel 1869 F A F T K R V L G E S G E M D A L R I Q

Query: 5928 gatggaagagcgattcatggcttccaatccttccaaggtctcctatcagccaatcactac 5987  
|||||  
Sbjct: 5915 gatggaagaaaaggttcatggcttccaacccctccaaggtctcctatcagccaatcactac 5974  
Na+ channel 1889 M E E R F M A S N P S K V S Y Q P I T T

Query: 5988 tactttaaaacgaaaacaagaggaagtatctgctgtcattattcagcgtgcttacagacg 6047  
|| |||||  
Sbjct: 5975 aacgttaaaaacgaaagcaagaggaggtgtcagccgttatcattcagcgtgcttacaggcg 6034  
Na+ channel 1909 T L K R K Q E E V S A V I I Q R A Y R R

Query: 6048 ccaccttttaagcggaactgtaaaacaagcttctttacgtacaataaaaaacaaatcaa 6107  
|||||  
Sbjct: 6035 ccaccttttgaagcggaacagtaaaaacaagcttcattcacatacaataagaacaaactcaa 6094  
Na+ channel 1929 H L L K R T V K Q A S F T Y N K N K L K

Query: 6108 aggtggggctaatacttcttataaaaagaagacatgataattgacagaataaatgaaaactc 6167  
|| |||||  
Sbjct: 6095 gggcggggctaatacttcttgtaaaagaagacatgatcattgacaggataaatgaaaactc 6154  
Na+ channel 1949 G G A N L L V K E D M I I D R I N E N S

Query: 6168 tattacagaaaaaactgatctgaccatgtccactgcagcttgtccaccttcctatgaccg 6227  
|||||  
Sbjct: 6155 tattacagagaaaactgacctgacgatgtccactgcagcttgtccgcctcctacgaccg 6214  
Na+ channel 1969 I T E K T D L T M S T A A C P P S Y D R

Query: 6228 ggtgacaaagccaattgtggaaaaacatgagcaagaaggcaaagatgaaaaagccaaagg 6287  
|||||  
Sbjct: 6215 ggtgacaaagccaatcgtggagaaacacgagcaggaaggaaaagatgagaaagccaaagg 6274  
Na+ channel 1989 V T K P I V E K H E Q E G K D E K A K G

Query: 6288 gaaataaatgaaaataaataaaaa-----taattgggtgacaaattgtttacagcctgtg 6342  
|||||  
Sbjct: 6275 gaaatgaacacaaacaaacaaaaataataaattgggtgacaaattgtttacagcctgtg 6334

Score = 854 bits (444), Expect = 0.0  
Identities = 743/870 (85%), Gaps = 14/870 (1%)  
Strand = Plus / Plus



Query: 7692 tgtttagaattttataagcaaataataat-actgtaaaaagtcactttattttatttttc 7750

Sbjct: 6580 gggg--ggttaacgtgaaacacttttagtgtagtaactgtattcaccgtttgcatttcaa 6636

Query: 6660 ctgccacatttgtcacatttt-tatggaatctgttagtggaattcatcttttttggt-aatc 6717  
|||||  
Sbjct: 6637 ctgccacatttgtcaggtttgtacaaactctgttagtggaattcatcttttttttaaate 6696

Query: 6718 cat---gtgtttatttatatgtgactatttttgtaaacgaagtttctgttgagaaataggc 6774  
|||  
Sbjct: 6697 catatgttgtttgttacatgtgactatttttgtaaacggggtttctgttgaggaaacagac 6756

Query: 6775 t-aaggacctctataacaggtatgccacctggggggtatggcaaccacatggccctccca 6833  
|  
Sbjct: 6757 taaaggaactcttttcctgtgtgtcacctgggggtattgacatccatacagccctccca 6816

Query: 6834 gctacacaaagtcgtgg-tttgca--tgagggcacgtgcacttagagatcatgcatgag 6890  
||  
Sbjct: 6817 tctgcacaacgatgtggttttgcacgtgagggcacgtgtaccttacgatcatgcatgag 6876

Query: 6891 -aaaaagtcacaagaaaaacaaa 6912  
|||  
Sbjct: 6877 aaaaaagtcacaaggaaagcaaa 6899

Score = 166 bits (86), Expect = 9e-37  
Identities = 232/290 (80%), Gaps = 11/290 (3%)  
Strand = Plus / Plus

Query: 8097 ttttcatttctttggagtaatgctgctctag-ttgttctaaatagaat-gtgggcttcat 8154  
|||  
Sbjct: 8112 ttttctttgctttggaatcacgcacatctctagattgttctaaatataaacgtgagcttcgg 8171

Query: 8155 aatttttttttc-cacaaaaacagagtagtcaacttatatagtcattacatcaggacat 8213  
|||  
Sbjct: 8172 aatttcttttctcctcaaaaacagagaggatgacacttacatagtcattatatcaagatat 8231

Query: 8214 tttgtgtttcttacagaagcaaacataggctcctcttttccttaa-----aactactt 8267  
||  
Sbjct: 8232 tt-gtgtttcttacagaagcagaccataggcacctctttttcttaagaaaaaaatattt 8290

Query: 8268 agataaactgtattcgtgaactgcatgctggaaaatgctactattatgctaaataatgct 8327  
||  
Sbjct: 8291 aggcaaacctgattcatgaactgcatgttggaaaatgctactattgccccaaatgatgct 8350

Query: 8328 aaccaacatttaaaatgtgcaaaactaataaagattacattttttatttt 8377  
||  
Sbjct: 8351 aatcacaattaaaaatgtgcaaatctaataaaaatta-attttttatttt 8399

Score = 102 bits (53), Expect = 1e-17  
Identities = 123/148 (83%), Gaps = 11/148 (7%)  
Strand = Plus / Plus

97  
98

Query: 1 tactgcagaggtctctggtgcatgtgtgtatgtgtgcgtttgtgtgtgtttgtgtgtctg 60  
|||||  
Sbjct: 1 tactgcagaggtctctggtgcatgtgtatgtgtgtgc-----gtgtgtt--tgtgtacg 52

Query: 61 tgtgttctgccccagtgagactgcagcccttgt-aaatactttgacaccttttgcaagaa 119  
|  
Sbjct: 53 tatgttctgccccctgtcaggctgcagcccttgtgaaacacttggtcaccttttgcaagaa 112

Query: 120 ggaa--tctgaacaattgcaactgaagg 145  
|||  
Sbjct: 113 ggaatctctgaatcgttgcaactgaagg 140

Score = 56.4 bits (29), Expect = 0.001  
Identities = 35/38 (92%)  
Strand = Plus / Plus

Query: 7036 tcttagcaggtgcaaacttcattcaaagtgttgagtc 7073  
|||||  
Sbjct: 7054 tcttagtaggtgcaaacttcattcaaagtgttgagtc 7091

CPU time: 0.08 user secs. 0.00 sys. secs 0.08 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 95  
Number of Sequences: 0  
Number of extensions: 95  
Number of successful extensions: 37  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 9  
length of query: 8378  
length of database: 10,761,364,081  
effective HSP length: 27  
effective length of query: 8351  
effective length of database: 10,761,364,054  
effective search space: 89868151214954  
effective search space used: 89868151214954  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)

S1: 12 (23.8 bits)  
S2: 23 (44.9 bits)



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## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

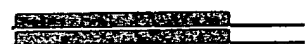
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

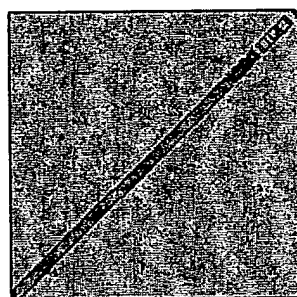
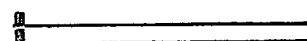
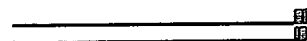
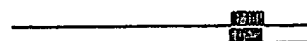
Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 gi 14545111 Sequence 2 from Patent WO0138564. Length 8378 (1 .. 8378)

Sequence 2 gi 1041088 Rattus norvegicus sodium channel I mRNA, complete cds. Length 8399 (1 .. 8399)



2

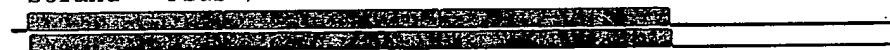


1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 8077 bits (4201), Expect = 0.0  
 Identities = 5475/6107 (89%), Gaps = 2/6107 (0%)  
 Strand = Plus / Plus



Query: 169 gggatgatgctgttcctcactgcagatggataatcttcttttaatacaggaatttcataatg 228

Sbjct: 155 gggagatgttgcttccttactgcagatagataatcttcttttatcaggaatctcacatg 214

Query: 229 cagaataaatggtaattaaaatgtgcaggatgacaagatggagcaaacagtgcttgatgacc 288

Sbjct: 215 aagagtaaagagtaattaaaatgtgcaggatgacaagatggagcaaacagtgcttgatgacc 274  
 Na+ channel 1 M E Q T V L V P

Query: 289 accaggacctgacagcttcaacttcttcaccagagaatctcttgaggctattgaaagacg 348

Sbjct: 275 ||||| accaggacctgacagcttcaacttcttcaccagagaatctcttgacagctattgaaagggcg 334  
Na+ channel 9 P G P D S F N F F T R E S L A A I E R R

Query: 349 cattgcagaagaaaaggcaaagaatcccaaaccagacaaaaaagatgacgacgaaaatgg 408  
Sbjct: 335 ||||| cattgcagaagaaaagctaagaatcccaagccagacaaaaaagatgatgatgaaaatgg 394  
Na+ channel 29 I A E E K A K N P K P D K K D D D E N G

Query: 409 cccaaagccaaatagtgacttggaagctggaaagaaccttccattttatgttgagacat 468  
Sbjct: 395 ||||| cccaaagccgaacagtgacttggaagctgggaagaaccttccattttatctatggagacat 454  
Na+ channel 49 P K P N S D L E A G K N L P F I Y G D I

Query: 469 tcctccagagatgggtgtcagagccctggaggacctggacccctactatatcaataagaa 528  
Sbjct: 455 ||||| tcctccagagatgggtgtcggagcctctggaggacctggacccctactatatcaataagaa 514  
Na+ channel 69 P P E M V S E P L E D L D P Y Y I N K K

Query: 529 aacttttatagtagtattgaataaagggaaggccatcttccggttcagtgccacctctgccct 588  
Sbjct: 515 ||||| aacttttatagtagtattgaataaagggaaggccatcttccggttcagtgccacctctgccct 574  
Na+ channel 89 T F I V L N K G K A I F R F S A T S A L

Query: 589 gtacattttaactcccttcaatcctcttaggaaaaatagctattaagattttggtacattc 648  
Sbjct: 575 ||||| gtacattttaactcccttcaatcctcttaggaaaaatagctattaagattttggtacactc 634  
Na+ channel 109 Y I L T P F N P L R K I A I K I L V H S

Query: 649 attattcagcatgctaattatgtgcactattttgacaaactgtgtgtttatgacaatgag 708  
Sbjct: 635 ||||| attattcagcatgttaattatgtgcactattttgacgaactgtgtattttatgacaatgag 694  
Na+ channel 129 L F S M L I M C T I L T N C V F M T M S

Query: 709 taaccctcctgattggacaaagaatgtagaatacaccttcacaggaatatatacttttga 768  
Sbjct: 695 ||||| taaccctcctgactggacaaagaatgtagagtacaccttcacaggaatatatacttttga 754  
Na+ channel 149 N P P D W T K N V E Y T F T G I Y T F E

Query: 769 atcacttataaaaaattattgcaaggggattctgtttagaagattttactttccttcggga 828  
Sbjct: 755 ||||| atcactaataaaaaattattgcaaggggcttctgtttagaagattttactttccttcgtga 814  
Na+ channel 169 S L I K I I A R G F C L E D F T F L R D

Query: 829 tccatggaactggctcgatttcactgtcattacatttgcggttgtaacagaatttgtaaa 888  
Sbjct: 815 ||||| cccatggaactggctggacttcactgtcattacatttcgcatatgtgacggagtttggtga 874  
Na+ channel 189 P W N W L D F T V I T F A Y V T E F V D

Query: 889 cctaggcaatttttcagctcttcgcacttttcagagtccttgagagctttgaaaactatttc 948

|||||  
Sbjct: 875 cctgggcaatgtctcagcggttgagaacattcagagttcttcgagcattgaaaacaatatc 934  
Na+ channel 209 L G N V S A L R T F R V L R A L K T I S

Query: 949 ggtaattccaggcctgaaaaccattgtgggagccctgatccagtcctgtgaagaagctctc 1008  
|||  
Sbjct: 935 agtcattccaggcctgaagaccatcggtggggccctgatccagtcctgtgaagaagctctc 994  
Na+ channel 229 V I P G L K T I V G A L I Q S V K K L S

Query: 1009 agatgtaatgatcctgactgtgttctgtctgagcgtatttgctctaattgggctgcagct 1068  
|||  
Sbjct: 995 tgacgtcatgatcctcaccgtgttctgtctcagtggtttgctctaattcggttgcagct 1054  
Na+ channel 249 D V M I L T V F C L S V F A L I G L Q L

Query: 1069 gttcatgggcaacctgaggaataaatgtatacaatggcctcccaccaatgcttccttga 1128  
|||||  
Sbjct: 1055 tttcatgggcaacctgaggaataagtgtgtacagtggccccccaccaacgcttccttga 1114  
Na+ channel 269 F M G N L R N K C V Q W P P T N A S L E

Query: 1129 ggaacatagtatagaaaaagaatataactgtgaattataatggtacacttataaatgaaac 1188  
|||||  
Sbjct: 1115 ggaacatagcatagagaagaatgtaactacggattacaacggcacacttgtaaatgaaac 1174  
Na+ channel 289 E H S I E K N V T T D Y N G T L V N E T

Query: 1189 tgtctttgagtttgactggaagtcatatattcaagattcaagatatcattatttccttga 1248  
|||  
Sbjct: 1175 cgtgtttgaatttgactggaaatcatacattcaagactcaagatatcattatttccttga 1234  
Na+ channel 309 V F E F D W K S Y I Q D S R Y H Y F L E

Query: 1249 ggggttttttagatgcactactatgtggaaatagctctgatgcaggccaatgtccagaggg 1308  
|||||  
Sbjct: 1235 ggggtgttttagatgcactactgtgtggaaatagctctgatgcaggccaatgtccagaagg 1294  
Na+ channel 329 G V L D A L L C G N S S D A G Q C P E G

Query: 1309 atatatgtgtgtgaaagctggtagaaatcccaattatggctacacaagctttgatacctt 1368  
|||  
Sbjct: 1295 ttacatgtgtgtgaaaagctggcagaaaccctaactatggttacacaagctttgacacctt 1354  
Na+ channel 349 Y M C V K A G R N P N Y G Y T S F D T F

Query: 1369 cagttgggcttttttgccttgtttcgactaatgactcaggacttctgggaaaatcttta 1428  
|||||  
Sbjct: 1355 cagctgggcattttctgtccctgtttcgactgatgactcaggacttctgggaaaatcttta 1414  
Na+ channel 369 S W A F L S L F R L M T Q D F W E N L Y

Query: 1429 tcaactgacattacgtgctgctgggaaaacgtacatgatatttttgtattggtcatttt 1488  
|||||  
Sbjct: 1415 ccaactgacattgctgctgcccgggaaaacatacatgatatttttgtgctggtcatttt 1474  
Na+ channel 389 Q L T L R A A G K T Y M I F F V L V I F

Query: 1489 cttgggctcattctacctaataaatttgatcctggctgtgggtggccatggcctacgagga 1548

Query: 2088 gtttqtgccccgacgacacggagagagacgcaacagcaacctgagtcagaccagtaggtc 2147

Query: 2688 tgggatctttacagcagaaatgtttctgaaaattattgccatggatccttactattattt 2747

|||||  
Sbjct: 2675 tgggatcttcacagcagaaatgttcctgaaaatcattgccatggacccttactattattt 2734  
Na+ channel 809 G I F T A E M F L K I I A M D P Y Y Y F

Query: 2748 ccaagaaggctggaatatctttgacggttttattgtgacgcttagcctggtagaacttgg 2807  
|||||  
Sbjct: 2735 ccaagagggctggaatatctttgatggtttcattgtgacactcagcctggtagaacttgg 2794  
Na+ channel 829 Q E G W N I F D G F I V T L S L V E L G

Query: 2808 actcgccaatgtggaaggattatctgttctccgttcatttcgattgctgcgagttttcaa 2867  
||  
Sbjct: 2795 ccttgccaatgtggaagggttatcagttctccgttcattccgactgctccgagttttcaa 2854  
Na+ channel 849 L A N V E G L S V L R S F R L L R V F K

Query: 2868 gttggcaaaatcttggccaacgttaaataatgctaataaagatcatcggaattccgtggg 2927  
|||||  
Sbjct: 2855 gttggcaaagtcctggcccacactgaacatgctcattaagatcatcggaactcggtggg 2914  
Na+ channel 869 L A K S W P T L N M L I K I I G N S V G

Query: 2928 ggctctgggaaatttaaccctcgtcttggccatcatcgtcttcatttttggcgtgggtcgg 2987  
||  
Sbjct: 2915 cgcactgggcaacctgacctgggtgctggccatcatcgtcttcatttttggcgtgggtcgg 2974  
Na+ channel 889 A L G N L T L V L A I I V F I F A V V G

Query: 2988 catgcagctcttttggtaaaagctacaaagattgtgtctgcaagatcgccagtgtgtca 3047  
|||||  
Sbjct: 2975 catgcagctgttcggcaaaagttacaaagattgtgtctgcaaaattgccactgactgcaa 3034  
Na+ channel 909 M Q L F G K S Y K D C V C K I A T D C K

Query: 3048 actcccacgctggcacatgaatgacttcttccactccttctctgattgtgttccgcgtgct 3107  
|||||  
Sbjct: 3035 actcccgcgctggcacatgaacgacttcttccactccttctctgactgtgttccgagtgt 3094  
Na+ channel 929 L P R W H M N D F F H S F L I V F R V L

Query: 3108 gtgtggggagtggtatagagaccatgtgggactgtatggaggttgctggtcaagccatgtg 3167  
|||||  
Sbjct: 3095 gtgtggggagtggtatagagaccatgtgggactgcatggaggtcgcggtcaagccatgtg 3154  
Na+ channel 949 C G E W I E T M W D C M E V A G Q A M C

Query: 3168 ccttactgtcttcatgatgggtcatgggtgattggaaacctagtggctcctgaatctctttct 3227  
|||||  
Sbjct: 3155 ccttactgtcttcatgatgggtcatgggtgattaggaaccttggtgctcctgaacctctttct 3214  
Na+ channel 969 L T V F M M V M V I R N L V V L N L F L

Query: 3228 ggccttgcttctgagctcatttagtgcagacaaccttgagccactgatgatgataatga 3287  
|||||  
Sbjct: 3215 ggccttgcttctgagctcatttagtgcagacaaccttgagccactgacgatgacaacga 3274  
Na+ channel 989 A L L L S S F S A D N L A A T D D D N E

Query: 3288 aatgaataatctccaaattgctgtggataggatgcacaaaggagtagcttatgtgaaaag 3347

Sbjct: 3275 aatgaacaaccttcaaattgctgtggacaggatgcacaaaggagtagcttatgtaaaaag 3334  
Na+ channel 1009 M N N L Q I A V D R M H K G V A Y V K R

Query: 3348 aaaaatatatgaatttattcaacagtccttcattaggaacaaaagatttttagatgaaat 3407  
Sbjct: 3335 aaaaatatatgagtttattcaacagtcctttgtaggaacagagaagatccttagatgaaat 3394  
Na+ channel 1029 K I Y E F I Q Q S F V R K Q K I L D E I

Query: 3408 taaccacttgatgatctaacaacaagaaagacagttgtatgtccaatcatacagcaga 3467  
Sbjct: 3395 taagccacttgatgatctaacaacagaaaagacaattgtacatctaaccacacgacaga 3454  
Na+ channel 1049 K P L D D L N N R K D N C T S N H T T E

Query: 3468 aattgggaaagatcttgactatcttaagatgtaaatggaactacaagtggataggaac 3527  
Sbjct: 3455 gattgggaaagatctggactgtctgaaagatgtgaatggaaccacgagtggtatagggac 3514  
Na+ channel 1069 I G K D L D C L K D V N G T T S G I G T

Query: 3528 tggcagcagtggtgaaaaatacattattgatgaaagtgattacatgtcattcataaaca 3587  
Sbjct: 3515 cggcagcagtggtgaaaagtacatcattgatgagagtgtactacatgtcattcataaaca 3574  
Na+ channel 1089 G S S V E K Y I I D E S D Y M S F I N N

Query: 3588 cccagtccttactgtgactgtaccaattgctgtaggagaatctgactttgaaaatttaa 3647  
Sbjct: 3575 cccagcctcaccgtgactgtgccattgctgtgggagagtctgactttgaaaacttaa 3634  
Na+ channel 1109 P S L T V T V P I A V G E S D F E N L N

Query: 3648 cacggaagacttttagtagtgaatcggatctggaagaaagcaaagagaaactgaatgaaag 3707  
Sbjct: 3635 cacagaggacttttagcagtgaatcagatctagaagaaagcaaagagaaactcaacgaaag 3694  
Na+ channel 1129 T E D F S S E S D L E E S K E K L N E S

Query: 3708 cagtagctcatcagaaggtagcactgtggacatcggcgacactgtagaagaacagcccgt 3767  
Sbjct: 3695 cagtagttcctcagaaggaagcacagtagacatcggggcgacctgaggagaaacagcctgt 3754  
Na+ channel 1149 S S S S E G S T V D I G A P A E E Q P V

Query: 3768 agtggaaacctgaagaaactcttgaaaccagaagcttgtttcactgaaggctgtgtacaaag 3827  
Sbjct: 3755 catggaaccagaagaaacccttgagcccgaagcttgcctcactgaaggctgtgtgcagag 3814  
Na+ channel 1169 M E P E E T L E P E A C F T E G C V Q R

Query: 3828 attcaagtgttgtaaataaatgtggaagaaggcagaggaaaacaatggtggaacctgag 3887  
Sbjct: 3815 attcaagtgttgtaaataaatcagtggtggaagaaggagaaaacagtggtggaaccttcg 3874  
Na+ channel 1189 F K C C Q I S V E E G R G K Q W W N L R

Query: 3888 aaggacgtgtttccgaatagttgaacataactggtttgagaccttcattgttttcattgat 3947

Sbjct: 3875 gagaacgtgcttccgaatagttgagcacaactgggttgagaccttcattgtgttcgat 3934  
Na+ channel 1209 R T C F R I V E H N W F E T F I V F M I

Query: 3948 tctccttagtagtggtgctctggcatttgaagatatatatattgatcagcgaaagacgat 4007  
Sbjct: 3935 tctcctcagtagtggtgccctggcctttgaggatatatacattgatcagcgaaagacaat 3994  
Na+ channel 1229 L L S S G A L A F E D I Y I D Q R K T I

Query: 4008 taagacgatgttggaatatgctgacaagggttttcacttacattttcattctggaaatgct 4067  
Sbjct: 3995 caagaccatgctggagtatgcagacaagggttttcacttacattttatcctggagatgct 4054  
Na+ channel 1249 K T M L E Y A D K V F T Y I F I L E M L

Query: 4068 tctaaaatgggtggcatatggctatcaaaa-tatttcaccaatgcctgggtgttggtgga 4126  
Sbjct: 4055 cctcaaatgggtagcctacggctatcaaacgtatttcaccaatgcctgggtgttggtgga 4114  
Na+ channel 1269 L K W V A Y G Y Q T Y F T N A W C W L D

Query: 4127 cttcttaattgttgatgtttcattgggtcagtttaacagcaaatgccttgggttactcaga 4186  
Sbjct: 4115 cttcttaattgttgatgtttcattgggtcagtttaacagcaaatgccttgggttactctga 4174  
Na+ channel 1289 F L I V D V S L V S L T A N A L G Y S E

Query: 4187 acttggagccatcaaattctctcaggacactaagagctctgagacctctaagagccttatc 4246  
Sbjct: 4175 acttggggccatcaagtccttaaggacactaagagctctgagacccttaagagccttatc 4234  
Na+ channel 1309 L G A I K S L R T L R A L R P L R A L S

Query: 4247 tcgatttgaagggatgaggggtggttgatgaatgcccttttaggagcaattccatccatcat 4306  
Sbjct: 4235 acgatttgaagggatgaggggtggttgatgaatgccctgttaggagcaattccatccatcat 4294  
Na+ channel 1329 R F E G M R V V V N A L L G A I P S I M

Query: 4307 gaatgtgcttctggtttgtcttatattctggctaattttcagcatcatgggcgtaaat 4366  
Sbjct: 4295 gaatgtgcttctggtttgccttatattctggctaattttcagcatcatgggcgtaaat 4354  
Na+ channel 1349 N V L L V C L I F W L I F S I M G V N L

Query: 4367 gtttgctggcaaattctaccactgtattaacaccacaactggtgacaggtttgacatcga 4426  
Sbjct: 4355 gtttgctggcaaattctaccactgtgttaacaccacaactggtgacacatttgagatcac 4414  
Na+ channel 1369 F A G K F Y H C V N T T T G D T F E I T

Query: 4427 agacgtgaataatcatactgattgcctaaaactaatagaaagaaatgagactgctcgatg 4486  
Sbjct: 4415 cgaagtcaataatcattctgattgcctaaaactaatagaaagaaatgagactgcccgggtg 4474  
Na+ channel 1389 E V N N H S D C L K L I E R N E T A R W

Query: 4487 gaaaaatgtgaaagtaaactttgataatgtaggatttgggtatctctctttgcttcaagt 4546



Sbjct: 4475 gaaaaatgtgaaagtaaacttttgataatgtaggatttgggtatctttctttgcttcaagt 4534  
Na+ channel 1409 K N V K V N F D N V G F G Y L S L L Q V

Query: 4547 tgccacattcaaaggatggatggatataatgtatgcagcagttgattccagaaatgtgga 4606  
Sbjct: 4535 tgcgacgtttaagggttggatggatatcatgtatgcagcagttgattccagaaatgtgga 4594  
Na+ channel 1429 A T F K G W M D I M Y A A V D S R N V E

Query: 4607 actccagcctaagtatgaagaaagtctgtacatgtatctttactttgttattttcatcat 4666  
Sbjct: 4595 actgcagcctaagtatgaggaaagcctgtacatgtacctgtacttcgtcatcttcatcat 4654  
Na+ channel 1449 L Q P K Y E E S L Y M Y L Y F V I F I I

Query: 4667 ctttgggtccttcttcaccttgaacctgtttattgggtgtcatcatagataatttcaacca 4726  
Sbjct: 4655 cttcggtcgttcttctactctaaatctattcatcggtgtcatcatagacaacttcaacca 4714  
Na+ channel 1469 F G S F F T L N L F I G V I I D N F N Q

Query: 4727 gcagaaaaagaagtttggaggtcaagacatctttatgacagaagaacagaagaataacta 4786  
Sbjct: 4715 gcagaagaagaagtttggaggtcaagacatctttatgacagaagaacagaagaataacta 4774  
Na+ channel 1489 Q K K K F G G Q D I F M T E E Q K K Y Y

Query: 4787 taatgcaatgaaaaaattaggatcgaaaaaacgcctatacctcgaccaggaaa 4846  
Sbjct: 4775 taatgcaatgaagaaattaggatcaaaaaagccacaaaagcctatccctcgacctggaaa 4834  
Na+ channel 1509 N A M K K L G S K K P Q K P I P R P G N

Query: 4847 caaatttcaaggaatgggtctttgacttcgtaaccagacaagtttttgacataagcatcat 4906  
Sbjct: 4835 caaatttcaaggaatgggtctttgactttgtaaccagacaagtgtttgacatcagcatcat 4894  
Na+ channel 1529 K F Q G M V F D F V T R Q V F D I S I M

Query: 4907 gattctcatctgtcttaacatgggtcacatgatgggtggaaacagatgaccagagtgaata 4966  
Sbjct: 4895 gatcctcatctgtctgaacatgggtgacctgatgggtggaaacggatgaccagagcgatta 4954  
Na+ channel 1549 I L I C L N M V T M M V E T D D Q S D Y

Query: 4967 tgtgactaccattttgtcacgcatcaatctgggtgttcattgtgctattttactggagagtg 5026  
Sbjct: 4955 tgtgacaagcattttgtcacgtatcaacctgggtgttcattgtgctgttcaccggcgagtg 5014  
Na+ channel 1569 V T S I L S R I N L V F I V L F T G E C

Query: 5027 tgtactgaaactcatctctctacgccattattattttaccattggatggaatatttttga 5086  
Sbjct: 5015 cgtgctgaagctcatctccctccgccattattattttaccattggctggaatatttttga 5074  
Na+ channel 1589 V L K L I S L R H Y Y F T I G W N I F D

Query: 5087 ttttgtggttgtcattctctccattgtaggtatgtttcttgccgagctgatagaaaagta 5146

Query: 5687 ctatgagggtttgggagaaagtattgatcccgatgcaactcagttcatggaatttgaaaaatt 5746

|||||  
Sbjct: 5675 ctacgaggtctgggagaagttcgaccctgacgccactcagttcatggaatttgaaaaatt 5734  
Na+ channel 1809 Y E V W E K F D P D A T Q F M E F E K L

Query: 5747 atctcagtttgagctgctgaaccgcctctcaatctgccacaaccaaaactcca 5806  
|||||

Sbjct: 5735 atctcagtttgagctgctgaacccctctcaactaccacaaccgaacaaacttca 5794  
Na+ channel 1829 S Q F A A A L E P P L N L P Q P N K L Q

Query: 5807 gctcattgccatggatttgcccatggtgagtggtgaccggatccactgtcttgatatctt 5866  
|||||

Sbjct: 5795 gctcattgccatggacctgcccatggtgagtggtgaccggatccactgtcttgatatctt 5854  
Na+ channel 1849 L I A M D L P M V S G D R I H C L D I L

Query: 5867 atttgctttttacaaagcgggttctaggagagagtggtgagagatggatgctctacgaataca 5926  
|||||

Sbjct: 5855 gtttgctttttacaaagcgggttctggcgagagtggtgagagatggacgctcttcgaatcca 5914  
Na+ channel 1869 F A F T K R V L G E S G E M D A L R I Q

Query: 5927 gatggaagagcgttcatggcttccaatccttccaaggtctcctatcagccaatcactac 5986  
|||||

Sbjct: 5915 gatggaagaaaggttcatggcttccaacccctccaaggtctcctatcagccaatcactac 5974  
Na+ channel 1889 M E E R F M A S N P S K V S Y Q P I T T

Query: 5987 tacttttaaaacgaaaacaagaggaagtatctgctgtcattattcagcgtgcttacagacg 6046  
|||||

Sbjct: 5975 aacgtttaaaacgaaagcaagaggaggtgtcagccgttatcattcagcgcgttacaggcg 6034  
Na+ channel 1909 T L K R K Q E E V S A V I I Q R A Y R R

Query: 6047 ccaccttttaaaagcgaactgtaaaacaagcttctttacgtacaataaaaaacaaatcaa 6106  
|||||

Sbjct: 6035 ccaccttttgaagcgaacagtaaaaacaagcttcattcacatacaataagaacaaactcaa 6094  
Na+ channel 1929 H L L K R T V K Q A S F T Y N K N K L K

Query: 6107 aggtggggctaattcttcttataaaagaagacatgataattgacagaataaatgaaaactc 6166  
|||||

Sbjct: 6095 gggcggggctaattcttcttataaaagaagacatgatcattgacaggataaatgaaaactc 6154  
Na+ channel 1949 G G A N L L V K E D M I I D R I N E N S

Query: 6167 tattacagaaaaaactgatctgaccatgtccactgcagcttgccaccttcttatgaccg 6226  
|||||

Sbjct: 6155 tattacagagaaaaactgacctgacgatgtccactgcagcttgccgccttcttatgaccg 6214  
Na+ channel 1969 I T E K T D L T M S T A A C P P S Y D R

Query: 6227 ggtgacaaagccaattgtggaaaaacatgagcaagaaggcaaagatg 6273  
|||||

Sbjct: 6215 ggtgacaaagccaatcggtggagaaacacgagcaggaaggaaaagatg 6261  
Na+ channel 1989 V T K P I V E K H E Q E G K D

Score = 842 bits (438), Expect = 0.0  
Identities = 737/870 (84%), Gaps = 14/870 (1%)

Strand = Plus / Plus

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Query: 7157 gaattgacaaaattactctttataaatttctgcttttctgcactttgtttagccatc 7216  
|||||  
Sbjct: 7170 gaattgacaaaagaaccctttataaattcccgccttaaccctgcactttgtttagccatc 7229

Query: 7217 ttcggctctcagcaagggttgacactgta-tatgttaatgaaatgctatttattatgtaaa 7275  
|||  
Sbjct: 7230 ttcagctctcagcgagggttgacactgtaatgtgttaatgaaatgctatttattgtgtaaa 7289

Query: 7276 tagtcattttaccctgtggtgcacgtttgagcaaacaaataatgacctaagcacagtatt 7335  
|||||  
Sbjct: 7290 tagtcattttactctgtggtgcacgtttgagcaaacaaataatgacctaagcacagtatt 7349

Query: 7336 tattgcatcaaataatgtaccacaagaaatgtagagtgcagctttacacaggtaataaaa 7395  
|||||  
Sbjct: 7350 tattgcatcaaatacgtaccacgagaaacgtagagtgcagctgtccgctggtaataatac 7409

Query: 7396 tgtattctgtaccatttatagatagtttggtatgctatcaatgcatgtttatattaccatg 7455  
|||||  
Sbjct: 7410 tgtattctgtacca-ttatagatagtggtatgctgtcagtgcatgtcgatattaccatg 7468

Query: 7456 ctgctgtatctggtttctctcactgctcagaatctcat--ttatgagaaaccatatgtca 7513  
|||||  
Sbjct: 7469 ctgcggtatctagtttctcccaccactcagaatctcatactcatgagacaccatagggtca 7528

Query: 7514 gtggtaaagtcaaggaaattgttcaacagatctcatttattttaagtcattaagcaatagt 7573  
|||||  
Sbjct: 7529 gtggctaagtcaaggaaaccggttcagcagatttcatttctttaagtcattaagcaatagt 7588

Query: 7574 ttgcagcactttaacagctttttgggtattttttacattttaagtggataacatatgggtat 7633  
|||||  
Sbjct: 7589 ttgcagcattttaacaatgtctgggttgtttttcaattctaagtggatgacgttcaatgt 7648

Query: 7634 atagccagactgtacagacatgtttnnnnnnncac---actgcttaacctattaaatatg 7690  
|||||  
Sbjct: 7649 atagccagactgtacatacatgttcggaagacaacactactgcttaacctgttaaa-aca 7707

Query: 7691 tgtttagaattttataagcaaatataaat-actgtaaaaagtcactttattttatttttc 7749  
|||||  
Sbjct: 7708 tgtttagagttttataagcaagtataaataactgtacaaagtcactttcttttgttttc 7767

Query: 7750 agcattatgtacataaatatgaagaggaaattatcttcagggttgatatacacaatcacttt 7809  
|||||  
Sbjct: 7768 agcatcatgtac---atatgaagaggaaattatcttcagggttgatatacacgatcacttt 7823

Query: 7810 tcttactttctgtccatagtagtctttttcatgaaagaaatttgctaaataagacatgaaaa 7869  
|||||  
Sbjct: 7824 tcttactttccgtccacagcagttttttcatggaagatatttgctaactaagaaatgaaac 7883

Query: 7870 caagactgggtagttgtagatttctgcttttttaaattacatttgctaatttttagattatt 7929  
|||  
Sbjct: 7884 catgacgggtagtgtagatctctgcttttttaatacagggctttaagtttgattatt 7943

Query: 7930 tcacaattttaaggagcaaaaatagggttcacga-ttcatatccaaattatgcttttgcaatt 7988  
|||  
Sbjct: 7944 tcataattttaaggagcaaaagtacactcacaacctcacatccaaattatgatttgcaatt 8003

Query: 7989 ggaaaagggtttaaaattttatttatattt 8018  
|||  
Sbjct: 8004 gggaaaagggtagaacatttgatttatgttt 8033

Score = 452 bits (235), Expect = e-123  
Identities = 477/563 (84%), Gaps = 20/563 (3%)  
Strand = Plus / Plus

Query: 6364 aggactccttttaggaggtcaatgccaaactgactgtttttacacaaat-ctccttaaggt 6422  
|||||  
Sbjct: 6342 aggactccttttaggaagtcaatgccaaactgactgtttttacacaaattcactttaaggt 6401

Query: 6423 cagtgcctacaataagacagtgacccc-ttgtcagcaaact--gtgactctgtg-taaag 6478  
|||||  
Sbjct: 6402 cagtgcct-caataagacagtgacccccttgctcggaactctgtgactcttaggtaaag 6460

Query: 6479 gggagatgaccttgacaggaggttactgttctcactaccagctgacactgctgaagataa 6538  
|||||  
Sbjct: 6461 gggagatgaccttgacaggaggttactgttctcactaccagctgacactgctgaagacaa 6520

Query: 6539 gatgcacaatggctagtcagactgtagggaccagtttcaaggggtgcaaacctgtgattt 6598  
|||  
Sbjct: 6521 gagaca-aatggctatgcagactgtagggaccagcgtaaaggggtgcagagctataattt 6579

Query: 6599 tgggggtgtttaacatgaaacacttttagtgtagtaattgtatccactgtttgcatttcaa 6658  
|||  
Sbjct: 6580 gggg---gtttaacgtgaaacacttttagtgtagtaactgtattcaccgtttgcatttcaa 6636

Query: 6659 ctgccacatttgtcacatttt-tatggaatctgttagtggttcattctttttgtt-aatc 6716  
|||||  
Sbjct: 6637 ctgccacatttgtcaggttttgtacaaactctgttagtggttcattcttttttttaaatc 6696

Query: 6717 cat---gtggtttatttatatgtgactatttttgtaaacgaagtttctgttgagaaataggc 6773  
|||  
Sbjct: 6697 catatgttgtttgttacatgtgactatttttgtaaacggggttctgttgggaaacagac 6756

06/17/2004

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Query: 6315 tgggtgacaaattgtttacagcctgtgaag 6344

Sbjct: 6308 tgggtgacaaattgtttacagcctgtgaag 6337

Score = 56.4 bits (29), Expect = 0.001  
Identities = 35/38 (92%)  
Strand = Plus / Plus

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Query: 7035 tcttagcaggtgcaaacttcattcaaagtgttgagtc 7072

Sbjct: 7054 tcttagtaggtgcaaacttcattcaaagtgttgagtc 7091

CPU time: 0.10 user secs. 0.00 sys. secs 0.10 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 90  
Number of Sequences: 0  
Number of extensions: 90  
Number of successful extensions: 35  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 11  
length of query: 8378  
length of database: 10,761,364,081  
effective HSP length: 27  
effective length of query: 8351  
effective length of database: 10,761,364,054  
effective search space: 89868151214954  
effective search space used: 89868151214954  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 23 (44.9 bits)